

#6 PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/889,733

DATE: 12/19/2001
TIME: 15:54:47

Input Set : A:\SEQ LIST.txt
Output Set: N:\CRF3\12192001\I889733.raw

ENTERED

3 <110> APPLICANT: UNIVERSITY COLLEGE LONDON
 5 <120> TITLE OF INVENTION: DIMETHYLARGININE DIMETHYLAMINOHYDROLASES (as amended)
 7 <130> FILE REFERENCE: 117-358
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/889,733
 C--> 10 <141> CURRENT FILING DATE: 2001-11-19
 12 <150> PRIOR APPLICATION NUMBER: GB 9901705.5
 13 <151> PRIOR FILING DATE: 1999-01-26
 15 <150> PRIOR APPLICATION NUMBER: GB 9913066.8
 16 <151> PRIOR FILING DATE: 1999-06-04
 18 <160> NUMBER OF SEQ ID NOS: 13
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 858
 24 <212> TYPE: DNA
 25 <213> ORGANISM: H. Sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (1)..(858)
 31 <400> SEQUENCE: 1
 32 atg gcc ggc ctc ggc cac ccc tcc gcc ttc ggc cg^g gcc acc cac gcc 48
 33 Met Ala Gly Leu Gly His Pro Ser Ala Phe Gly Arg Ala Thr His Ala
 34 1 5 10 15
 36 gtg gtg cgg gcg cta ccc gag tcg ctc tgc cag cac g^c g^g ctg aga agc 96
 37 Val Val Arg Ala Leu Pro Glu Ser Leu Cys Gln His Ala Leu Arg Ser
 38 20 25 30
 40 gcc aag ggc gag gag gtg gac gtc gcc cgc g^c gaa cgg c^a g^g c^a c^a 144
 41 Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln
 42 35 40 45
 44 ctc tac gtg ggc gtg ctc ggc agc aag ctg ggg ctg cag gtg gtg gag 192
 45 Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu
 46 50 55 60
 48 ctg ccg gcc gac gag agc ctt ccg gac tgc gtc ttc gtg gag gac gtg 240
 49 Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val
 50 65 70 75 80
 52 gcc gtg tgc gag gag acg gcc ctc atc acc cga ccc ggg g^c g^g c^c 288
 53 Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro
 54 85 90 95
 56 agc cgg agg aag gag gtt gac atg atg aaa gaa gca tta gaa aaa ctt 336
 57 Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu
 58 100 105 110
 60 cag ctc aat ata gta gag atg aaa gat gaa aat gca act tta gat ggc 384
 61 Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly
 62 115 120 125
 64 gga gat gtt tta ttc aca ggc aga gaa ttt ttt gtg ggc ctt tcc aaa 432
 65 Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys
 66 130 135 140
 68 agg aca aat caa cga ggt gct gaa atc ttg gct gat act ttt aag gac 480

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69	Arg	Thr	Asn	Gln	Arg	Gly	Ala	Glu	Ile	Leu	Ala	Asp	Thr	Phe	Lys	Asp	
70	145				150				155				160				
72	tat	gca	gtc	tcc	aca	gtg	cca	gtg	gca	gat	ggg	ttg	cat	ttg	aag	agt	528
73	Tyr	Ala	Val	Ser	Thr	Val	Pro	Val	Ala	Asp	Gly	Leu	His	Leu	Lys	Ser	
74					165				170				175				
76	ttc	tgc	agc	atg	gct	ggg	cct	aac	ctg	atc	gca	att	ggg	tct	agt	gaa	576
77	Phe	Cys	Ser	Met	Ala	Gly	Pro	Asn	Leu	Ile	Ala	Ile	Gly	Ser	Ser	Glu	
78					180				185				190				
80	tct	gca	cag	aag	gcc	ctt	aag	atc	atg	caa	cag	atg	agt	gac	cac	cgc	624
81	Ser	Ala	Gln	Lys	Ala	Leu	Lys	Ile	Met	Gln	Gln	Met	Ser	Asp	His	Arg	
82					195				200				205				
84	tac	gac	aaa	ctc	act	gtg	cct	gat	gac	ata	gca	gca	aac	tgt	ata	tat	672
85	Tyr	Asp	Lys	Leu	Thr	Val	Pro	Asp	Asp	Ile	Ala	Ala	Asn	Cys	Ile	Tyr	
86					210				215				220				
88	cta	aat	atc	ccc	aac	aaa	ggg	cac	gtc	ttg	ctg	cac	cga	acc	ccg	gaa	720
89	Leu	Asn	Ile	Pro	Asn	Lys	Gly	His	Val	Leu	Leu	His	Arg	Thr	Pro	Glu	
90					225				230				235				240
92	gag	tat	cca	gaa	agt	gca	aag	gtt	tat	gag	aaa	ctg	aag	gac	cat	atg	768
93	Glu	Tyr	Pro	Glu	Ser	Ala	Lys	Val	Tyr	Glu	Lys	Leu	Lys	Asp	His	Met	
94					245				250				255				
96	ctg	atc	ccc	gtg	agc	atg	tct	gaa	ctg	gaa	aag	gtg	gat	ggg	ctg	ctc	816
97	Leu	Ile	Pro	Val	Ser	Met	Ser	Glu	Leu	Glu	Lys	Val	Asp	Gly	Leu	Leu	
98					260				265				270				
100	acc	tgc	tgc	tca	gtt	tta	att	aac	aag	aag	gta	gac	tcc	tga			858
101	Thr	Cys	Cys	Ser	Val	Leu	Ile	Asn	Lys	Lys	Val	Asp	Ser				
102					275				280				285				
105	<210>	SEQ ID NO:	2														
106	<211>	LENGTH:	285														
107	<212>	TYPE:	PRT														
108	<213>	ORGANISM:	H. Sapiens														
109	<400>	SEQUENCE:	2														
111	Met	Ala	Gly	Leu	Gly	His	Pro	Ser	Ala	Phe	Gly	Arg	Ala	Thr	His	Ala	
112		1			5				10				15				
114	Val	Val	Arg	Ala	Leu	Pro	Glu	Ser	Leu	Cys	Gln	His	Ala	Leu	Arg	Ser	
115					20				25				30				
117	Ala	Lys	Gly	Glu	Glu	Val	Asp	Val	Ala	Arg	Ala	Glu	Arg	Gln	His	Gln	
118					35				40				45				
120	Leu	Tyr	Val	Gly	Val	Leu	Gly	Ser	Lys	Leu	Gly	Leu	Gln	Val	Val	Glu	
121					50				55				60				
123	Leu	Pro	Ala	Asp	Glu	Ser	Leu	Pro	Asp	Cys	Val	Phe	Val	Glu	Asp	Val	
124					65				70				75				80
126	Ala	Val	Val	Cys	Glu	Glu	Thr	Ala	Leu	Ile	Thr	Arg	Pro	Gly	Ala	Pro	
127									85				90				95
129	Ser	Arg	Arg	Lys	Glu	Glu	Val	Asp	Met	Met	Lys	Glu	Ala	Leu	Glu	Lys	Leu
130									100				105				110
132	Gln	Leu	Asn	Ile	Val	Glu	Met	Lys	Asp	Glu	Asn	Ala	Thr	Leu	Asp	Gly	
133					115				120				125				
135	Gly	Asp	Val	Leu	Phe	Thr	Gly	Arg	Glu	Phe	Phe	Val	Gly	Leu	Ser	Lys	
136					130				135				140				

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Input Set : A:\SEQ_LIST.txt
Output Set: N:\CRF3\12192001\I889733.raw

138 Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp
139 145 150 155 160
141 Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser
142 165 170 175
144 Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu
145 180 185 190
147 Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg
148 195 200 205
150 Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr
151 210 215 220
153 Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu
154 225 230 235 240
156 Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met
157 245 250 255
159 Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu
160 260 265 270
162 Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser
163 275 280 285
167 <210> SEQ ID NO: 3
168 <211> LENGTH: 858
169 <212> TYPE: DNA
170 <213> ORGANISM: H. sapiens
172 <220> FEATURE:
173 <221> NAME/KEY: CDS
174 <222> LOCATION: (1)..(858)
176 <400> SEQUENCE: 3
177 atg ggg acg ccg ggg gag ggg ctg ggc cgc tgc tcc cat gcc ctg atc 48
178 Met Gly Thr Pro Gly Glu Gly Leu Gly Arg Cys Ser His Ala Leu Ile
179 1 5 10 15
181 cgg gga gtc cca gag agc ctg gcg tcg ggg gaa ggt gcg ggg gct ggc 96
182 Arg Gly Val Pro Glu Ser Leu Ala Ser Gly Glu Gly Ala Gly Ala Gly
183 20 25 30
185 ctt ccc gct ctg gat ctg gcc aaa gct caa agg gag cac ggg gtg ctg 144
186 Leu Pro Ala Leu Asp Leu Ala Lys Ala Gln Arg Glu His Gly Val Leu
187 35 40 45
189 gga ggt aaa ctg agg caa cga ctg ggg cta cag ctg cta gaa ctg cca 192
190 Gly Gly Lys Leu Arg Gln Arg Leu Gly Leu Gln Leu Leu Glu Leu Pro
191 50 55 60
193 cct gag gag tca ttg ccg ctg gga ccg ctg ctt ggc gac acg gcc gtg 240
194 Pro Glu Glu Ser Leu Pro Leu Gly Pro Leu Leu Gly Asp Thr Ala Val
195 65 70 75 80
197 atc caa ggg gac acg gcc cta atc acg cgg ccc tgg agc ccc gct cgt 288
198 Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg
199 85 90 95
201 agg cca gag gtc gat gga gtc cgc aaa gcc ctg caa gac ctg ggg ctc 336
202 Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu
203 100 105 110
205 cga att gtg gaa ata gga gac gag aac gcg acg ctg gat ggc act gac 384
206 Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp

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Input Set : A:\SEQ LIST.txt
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207	115	120	125	
209	gtt ctc ttc acc ggc cgg gag ttt ttc gta ggc ctc tcc aaa tgg acc			432
210	Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr			
211	130	135	140	
213	aat cac cga gga gct gag atc gtg gcg gac acg ttc cgg gac ttc gcc			480
214	Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala			
215	145	150	155	160
217	gtc tcc act gtg cca gtc tcg ggt ccc tcc cac ctg cgc ggt ctc tgc			528
218	Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys			
219	165	170	175	
221	ggc atg ggg gga cct cgc act gtt gtg gca ggc agc agc gac gct gcc			576
222	Gly Met Gly Pro Arg Thr Val Val Ala Gly Ser Ser Asp Ala Ala			
223	180	185	190	
225	caa aag gct gtc cgg gca atg gca gtg ctg aca gat cac cca tat gcc			624
226	Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala			
227	195	200	205	
229	tcc ctg acc ctc cca gat gac gca gct gct gac tgt ctc ttt ctt cgt			672
230	Ser Leu Thr Leu Pro Asp Asp Ala Ala Asp Cys Leu Phe Leu Arg			
231	210	215	220	
233	cct ggg ttg cct ggt gtg ccc cct ttc ctc ctg cac cgt gga ggt ggg			720
234	Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly Gly			
235	225	230	235	240
237	gat ctg ccc aac agc cag gag gca ctg cag aag ctc tct gat gtc acc			768
238	Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr			
239	245	250	255	
241	ctg gta cct gtg tcc tgc tca gaa ctg gag aaa gct ggc gcc ggg ctc			816
242	Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu			
243	260	265	270	
245	agc tcc ctc tgc ttg gtg ctc agc aca cgc ccc cac agc tga			858
246	Ser Ser Leu Cys Leu Val Leu Ser Thr Arg Pro His Ser			
247	275	280	285	
250	<210> SEQ ID NO: 4			
251	<211> LENGTH: 285			
252	<212> TYPE: PRT			
253	<213> ORGANISM: H. sapiens			
255	<400> SEQUENCE: 4			
256	Met Gly Thr Pro Gly Glu Gly Leu Gly Arg Cys Ser His Ala Leu Ile			
257	1	5	10	15
259	Arg Gly Val Pro Glu Ser Leu Ala Ser Gly Glu Gly Ala Gly Ala Gly			
260	20	25	30	
262	Leu Pro Ala Leu Asp Leu Ala Lys Ala Gln Arg Glu His Gly Val Leu			
263	35	40	45	
265	Gly Gly Lys Leu Arg Gln Arg Leu Gly Leu Gln Leu Leu Glu Leu Pro			
266	50	55	60	
268	Pro Glu Glu Ser Leu Pro Leu Gly Pro Leu Leu Gly Asp Thr Ala Val			
269	65	70	75	80
271	Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg			
272	85	90	95	
274	Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu			

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Input Set : A:\SEQ LIST.txt
Output Set: N:\CRF3\12192001\I889733.raw

275	100	105	110
277	Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp		
278	115	120	125
280	Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr		
281	130	135	140
283	Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala		
284	145	150	155
286	Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys		
287	165	170	175
289	Gly Met Gly Gly Pro Arg Thr Val Val Ala Gly Ser Ser Asp Ala Ala		
290	180	185	190
292	Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala		
293	195	200	205
295	Ser Leu Thr Leu Pro Asp Asp Ala Ala Asp Cys Leu Phe Leu Arg		
296	210	215	220
298	Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly		
299	225	230	235
301	240		
302	Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr		
304	245	250	255
305	Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu		
307	260	265	270
308	Ser Ser Leu Cys Leu Val Leu Ser Thr Arg Pro His Ser		
	275	280	285
312	<210> SEQ ID NO: 5		
313	<211> LENGTH: 777		
314	<212> TYPE: DNA		
315	<213> ORGANISM: S. coelicolor		
317	<220> FEATURE:		
318	<221> NAME/KEY: CDS		
319	<222> LOCATION: (1)..(777)		
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323	Val Pro Ser Lys Lys Ala Leu Val Arg Arg Pro Ser Pro Arg Leu Ala		
324	1	5	10
			15
326	15		
327	gaa gga ctg gtg aca cac gtc gag cgg gag cag gtc gat cac ggc ctg	96	
328	Glu Gly Leu Val Thr His Val Glu Arg Glu Gln Val Asp His Gly Leu		
329	20	25	30
330	30		
331	gcc ctc gaa cag tgg gac gcc tac gtc gag gcc ctc gga gca cac ggc	144	
332	Ala Leu Glu Gln Trp Asp Ala Tyr Val Glu Ala Leu Gly Ala His Gly		
333	35	40	45
334	45		
335	tgg gag act ctg gag gtg gac ccg gcc gag tac tgt ccg gac tcg gtc	192	
336	Trp Glu Thr Leu Glu Val Asp Pro Ala Glu Tyr Cys Pro Asp Ser Val		
337	50	55	60
338	60		
339	ttc gtc gag gac gcc gtc gtg ttc cgc aac gtc gcg ctg atc acg	240	
340	Phe Val Glu Asp Ala Val Val Phe Arg Asn Val Ala Leu Ile Thr		
341	65	70	75
			80
342	cgg ccc ggc gcc gag tcg cgg cgc gcg gag acg gcc ggc gtc gag gag	288	
343	Arg Pro Gly Ala Glu Ser Arg Arg Ala Glu Thr Ala Gly Val Glu Glu		
344	85	90	95

VERIFICATION SUMMARY

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Input Set : A:\SEQ LIST.txt

Output Set: N:\CRF3\12192001\I889733.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:866 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11

L:870 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11

L:874 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11